

Figure 1

Match 70 54, QCMATCH 68 44, MATCHES 572, CONSERVATIVE 105, MISMATCHES 111,
 INDELS 13, GAPS 5:

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2PEP_m      1  MDGRETLLQQLIKKAGKQKKNLSEFSEFSEFLGKQSTKPKAKIVPTITAGPPKIKKQRY 60
SuPTP04_h   1  MDGRETLLQVTLDEAGSKITKKEFSEFSEFLGKQSTKPKAKIVPTITAGPPKIKKQRY 60

2PEP_m      61  KDILFPTKSLVELSLTSCDESSVINASFIKGVGPKAYIATQQLSTTLDFPKRWKEY 120
SuPTP04_h   61  KDILFVGYSRVELSLTSCDESSVINASFIKGVGPKAYIATQQLSTTLDFPKRWKEY 120

2PEP_m      121  RILVIVMAQGEFEGKKKCKERYWAEPOETQLQFGPPSISCEAEKKSSDYKIRTLAKKPN 180
SuPTP04_h   121  RILVIVMAQGEFEGKKKCKERYWAEPOETQLQFGPPSISCEAEKKSSDYKIRTLAKKPN 180

2PEP_m      181  ETRITVQPHYQWPFCHVPSIDPILQLIWDRCYQEDDCVPICIKCSAGCGRTGVICAV 240
SuPTP04_h   181  ETRITVQPHYQWPFCHVPSIDPILQLIWDRCYQEDDCVPICIKCSAGCGRTGVICAV 240

2PEP_m      241  DVTWMLLKDGIIIPQTSVFNLIQEMRTQPSLVQTEQVELVYSAVLELFKRWVISEN 300
SuPTP04_h   241  DVTWMLLKDGIIIPQTSVFNLIQEMRTQPSLVQTEQVELVYSAVLELFKRWVIRCK 300

2PEP_m      301  HLGREYQAQCSIPBQSLTVEADSCPLDKPKAMRVKTTNHSKQGAPEASTGGSSLGRL 360
SuPTP04_h   301  HSGTESQAQHCIPBQSLTVEADSYSPNLKSTTKAAKQQAQQR---TQGLIKESSEFFR 357

2PEP_m      361  TSTNVAEELVLHSAKSSPSFNCLELAKGCKNKAVITRNGQARASPVUGEPQKYQSLDP 420
SuPTP04_h   358  TSEISAKDELVLHSAKSSSTSFDFLELANSFCKNADITKMQTKAFPIUGEFLQKHQSLDL 417

2PEP_m      421  GSKLFGSCPSALPINTADRYHNSKGPVKRTKSTPPELIQCRKTNDLAVGDQFSCLESQHL 480
SuPTP04_h   418  GSKLFGSCNSKPMNAAGRYFNKVPITRKTSTPPELIQCRKTEVDKSNFVLESQPH 477

2PEP_m      481  EHYSLRELQVRVAHVSSEELNYSLPGAC-----DASCVPRHSPGALRVMLYTSLAZPFY 535
SuPTP04_h   478  DSCFV-EMQACKVMHVSSEELNYSLPYDSKHQIRNASNVGHSIDSSALGVYSYIPLVETPFY 536

2PEP_m      536  FSSSPPTNSADSKQASFDLPEKQDQATSPQALLPASSTTSFFYSNPHOSLVMNTLSTSPPL 595
SuPTP04_h   537  FSSWPPSGTSSKQASLDLPEKQDQVTFPSILLPTSSTSLFSYNSHDSLENSPNTISLL 596

2PEP_m      596  NQETALEAPSRRTDDEIPPLPERTPEFIVVEAGEPSFRVIESLP--LWITGASPEC 651
SuPTP04_h   597  NQESAVLATAPRIDDEIPPLPVRTPEFIVVEAGEFSNNPKLSAASAKKIKGTSLFW 656

2PEP_m      654  GGTSEKSGVPTPSQKGLASPKSDRHQD-GSPPPPLPERTLESFPLADEDCQCAQ 711
SuPTP04_h   657  GGTSEPKGDDSVILRPSKSVKLRSKSELHQDRSGPPPLPERTLESFPLADEDCQCAQ 716

2PEP_m      712  AVQTSSTSYPTETENSTSSKQTLATPGKSPTRMSLXIFRNMCKSVNSSSPSKPIEVQ 771
SuPTP04_h   717  SIEVTSYSPVPTENSTSSKQTLATPGKSPTRKSLKILNKKKICNCSFNNKPAZSVQ 776

2PEP_m      772  PKISSSFLTFGGRNFSKPKGPRNPPPTANT 802
SuPTP04_h   777  SKISSSFLTFGGRNFSKPKGPRNPPPTANT 807

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